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OM nucleic - nucleic search, using sw model

Run on: April 4, 2003, 22:41:32 ; Search time 391 Seconds  
(without alignments)

9952.565 Million cell updates/sec  
1 agaaaccaggaaaacaac.....tcatcaaaccctcaaatggag 1728

Title: US-09-847-081B-1

Perfect score: 1728

Sequence: 1 agaaaccaggaaaacaac.....tcatcaaaccctcaaatggag 1728

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched: 2195239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:

4370478  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries  
N\_Geneseq\_1101002:  
1: /SIDS2/cgdata/geneseq/geneseq/geneseq-emb1/NA1980.DAT:\*

2: /SIDS2/cgdata/geneseq/geneseq/geneseq-emb1/NA1981.DAT:\*

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12: /SIDS2/cgdata/geneseq/geneseq/geneseq-emb1/NA1991.DAT:\*

13: /SIDS2/cgdata/geneseq/geneseq/geneseq-emb1/NA1992.DAT:\*

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17: /SIDS2/cgdata/geneseq/geneseq/geneseq-emb1/NA1996.DAT:\*

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24: /SIDS2/cgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1728	100.0	1728	24	AAI63366	Nicotiana tabacum
2	868	50.2	1826	19	AAV0880	Phytoene synthase
3	858.6	49.7	1795	19	AAV0878	Phytoene synthase
4	857.8	49.6	1712	24	AAI6367	Nicotiana tabacum
5	853.4	49.4	1814	19	AAV0881	Phytoene synthase
6	847.6	49.1	1591	17	AAQ09323	Melon phytoene-syn
7	840.4	48.6	1646	12	AAQ12495	Tomato fruit ripen
8	811.2	46.9	1316	19	AAV0879	Phytoene synthase
9	806.4	46.7	1239	21	AAZ9482	cDNA encoding a ph

/product= "phytoene synthase"

DE10022362-A1.

/product= "phytoene synthase"

AAQ29140

/product= "phytoene synthase"

AAQ29139

/product= "phytoene synthase"

AAQ29121

/product= "phytoene synthase"

AAH24248

/product= "phytoene synthase"

AAV0882

/product= "phytoene synthase"

AAB2143

/product= "phytoene synthase"

ABL1600

/product= "phytoene synthase"

AAQ29142

/product= "phytoene synthase"

AAZ29144

/product= "phytoene synthase"

AAZ29139

/product= "phytoene synthase"

AAV17247

/product= "phytoene synthase"

AAZ29146

/product= "phytoene synthase"

AAZ29145

/product= "phytoene synthase"

AAV16951

/product= "phytoene synthase"

AAV16949

/product= "phytoene synthase"

AAV16948

/product= "phytoene synthase"

AAV16950

/product= "phytoene synthase"

AAV16951

/product= "phytoene synthase"

AAV16952

/product= "phytoene synthase"

AAV16953

/product= "phytoene synthase"

AAV16954

/product= "phytoene synthase"

AAV16955

#### ALIGNMENTS

RESULT 1  
ID AA166366 standard; cDNA; 1728 BP.

AAI63366;

C 3.8

AAV0880

AAQ29140

AAQ29140

/product= "phytoene synthase"

AAQ29140

#### REFERENCES

RESULT 1  
ID AA166366 standard; cDNA; 1728 BP.

AAI63366;

C 3.8

AAV0880

AAQ29140

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RESULT 1  
ID AA166366 standard; cDNA; 1728 BP.

AAI63366;

C 3.8

AAV0880

AAQ29140

DR WPI; 2002-027336/04.  
 DR P-PDB; AAM51041.  
 XX New nucleic acid encoding tobacco zeta-carotene desaturase, useful for screening compounds with herbicidal activity -  
 PT  
 XX  
 PS Claim 14; Page 12-17; 44PP; German.  
 CC The present invention provides the protein and coding sequences of phytoene synthases and zeta-carotene desaturase from Nicotiana tabacum. The sequences can be used to identify compounds capable of altering the expression of these genes, which are therefore useful as plant growth regulators and herbicides. They can also be used to produce transgenic plants. The present sequence is the coding sequence of a tobacco phytoene synthase.  
 XX Sequence 1728 BP; 513 A; 290 C; 433 G; 492 T; 0 other;  
 SQ Query Match 100.0%; Score 1728; DB 24; Length 1728;  
 Best Local Similarity 100.0%; Prev. No. 0;  
 Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 AGAACCCAGAAAGAACACAGGTTGGGTACACTTCATATCGGATTTTAATCGGATAATTAGT 60  
 Qy 1 AGAACCCAGAAAGAACACAGGTTGGGTACACTTCATATCGGATTTTAATCGGATAATTAGT 60  
 Db 1 AGAACCCAGAAAGAACACAGGTTGGGTACACTTCATATCGGATTTTAATCGGATAATTAGT 60  
 Qy 61 GTGTAAAGCAGGTTGGGTACACTTCATATCGGATTTTAATCGGATAATTAGT 120  
 Db 61 GTGTAAAGCAGGTTGGGTACACTTCATATCGGATTTTAATCGGATAATTAGT 120  
 Qy 121 GATGACTCTAGTGATCATCTACAGATGTTTGATATAAAATAGCTGAGGTGAGA 180  
 Db 121 GATGACTCTAGTGATCATCTACAGATGTTTGATATAAAATAGCTGAGGTGAGA 180  
 Qy 181 AGGTACATAAGGAAGCAAAACTGGAAATTGTTAGACCGGGTTCTGT 240  
 Db 181 AGGTACATAAGGAAGCAAAACTGGAAATTGTTAGACCGGGTTCTGT 240  
 Qy 241 TTCAATGAGCATGTCGTTGGTTGGTTGGGGTTCTCGGAAT 300  
 Db 241 TTCAATGAGCATGTCGTTGGTTGGGGTTCTCGGAAT 300  
 Qy 301 GGGACAGGATTGGTGATCTAGTCGGAGGAAACCCGGCTCTGTATCCAGGTT 360  
 Db 301 GGGACAGGATTGGTGATCTAGTCGGAGGAAACCCGGCTCTGTATCCAGGTT 360  
 Qy 361 CTAGCTGAGATAGAATTTGATGGGAAATCAAGAAGGGTGGGACAANG 420  
 Db 361 CTAGCTGAGATAGAATTTGATGGGAAATCAAGAAGGGTGGGACAANG 420  
 Qy 421 TGGAAATTGGCTTAAATTGCTGATCAGAATGATTCTGCTGGGAGTAAGAAGCT 480  
 Db 421 TGGAAATTGGCTTAAATTGCTGATCAGAATGATTCTGCTGGGAGTAAGAAGCT 480  
 Qy 481 GAAAAGGGAAAGCAGCTTCCTGTCAGTCAGTCAGTTGGCTGAGCCACCTGGGAAATG 540  
 Db 481 GAAAAGGGAAAGCAGCTTCCTGTCAGTCAGTCAGTTGGCTGAGCCACCTGGGAAATG 540  
 Qy 541 ACTGGCTTGTGAGAACGATATGATGCCATTGTGGCAGTGGCAAGTATGCCAAG 720  
 Db 541 ACTGGCTTGTGAGAACGATATGATGCCATTGTGGCAGTGGCAAGTATGCCAAG 720  
 Qy 601 AGGAGCTGAGATCAAGGATTCAGCTGAGATGTTGGCTAGGGGATATTGGTCTCCAGGGAAAT 660  
 Db 601 AGGAGCTGAGATCAAGGATTCAGCTGAGATGTTGGCTAGGGGATATTGGTCTCCAGGGAAAT 660  
 Qy 661 TTGGCTTGTGAGAACGATATGATGCCATTGTGGCAGTGGCAAGTATGCCAAG 720  
 Db 661 TTGGCTTGTGAGAACGATATGATGCCATTGTGGCAGTGGCAAGTATGCCAAG 720  
 Qy 721 ACATTTACTTAGGACCAAGCTAATGACCCAGAGAGAAAGCTCTGGCAATA 780  
 Db 721 ACATTTACTTAGGACCAAGCTAATGACCCAGAGAGAAAGCTCTGGCAATA 780

RESULT 2  
 AAU03880 ID AAV03880 Standard; cDNA: 1826 BP.  
 XX  
 AC AAU03880;  
 DT 29-APR-1998 (first entry)



Db	308	TAAGGAAAAAACCTTGGATTGTTAGAACCAAGGTTTC -TTGTCAAGATGT	365
Qy	254	CTGTCTCTTGTGGGTTCTCCACACTTCGGGCTCGAATGGGACAGGATTGT	313
Db	366	CTGTCTCTTGTGGGTTCTCCAC---CTTGTAAGGTCAATGGGAGATTCT	422
Qy	314	TGGATTTCAGTCGAGGAAACGGGCTTGTATCATCAGGTCCTAGCTCGAGATA	373
Db	423	TGGATTCAATCGGGGGGARACGGGTTTGTATTGTCGAGGT-----ATA	470
Qy	374	GGAAATTGATGGGATGGGAGAACAGAAGGGGGAGACAAGGTGGGAATTCTGGCT	433
Db	471	GAAATTAGTGCATTGAGGAACAGAGGGTGGAAACAAAGTGGATTCTGG--	528
Qy	434	CTTAAATTGGTGTATCCAAGATTATCATGCTGGGTGATCAGAACTGAAAGGCCA	493
Db	529	-----	528
Qy	494	CTTTCTCTGTACAGTCAGTCAGCTGGGAAAT---GACTGCTCTAT	550
Db	529	---TCTCTTAAGGTCTGCTATGGGCTACCGGGGGAAATGGCAGCATGACAT	584
Qy	551	CAGAGAAAAAGGTGTATGTGGTATTAAGCAGGGCAGCTTGTAGAAGGGCACGTGA	610
Db	585	CAGAACAGATGGTTATGATGGTTAACAAAGCAGGTTAGAAGGGCAGTGA	644
Qy	611	GATCTACCGATGATTTGAAAGTGAACGGGATATGTTGTCAGGGAATTTGGCTGT	670
Db	645	GATCTACGTACTGATGATTTGAAACTGAACGGGGATCCCTCAGGGAAATTGGCTGT	704
Qy	671	TGAGTGAAGCATATGATGTTGCGGAAGTATGTTGAGATGAAAGACATTACT	730
Db	705	TGAGTGAAGCATATGATGGTGTAGTGAAGTATGTCAGAGTATGAAAGCATTTACT	764
Qy	731	TAGGAACCAACGTAATGACCCCAAGAGAAAGAACCTATCTGGCAATAATTGTTGGCT	790
Db	765	TAGGAACCATGCTTAATGACTCCAGAGAAAGGGCTATTGGCAATAATGATGTGGT	824
Qy	791	GCAGGGAACCGATGAGCTGTTGATGGCCCTAATGCATCCACATAACTCGCAAGCTT	850
Db	825	GCAGGGAACAGATGAGCTGTTGATGGCCCTAATGCATCCACATAACTCGCAAGCTT	884
Qy	851	TAGATAGCTGGAGACCGGGTGGAGATATTTCAGTGGGCCATTGATGCTTG	910
Db	885	TAGATAGTGGAAAGCCTGTTGAGATGTTTCAGTGGGCCATTGATGCTCG	944
Qy	911	ATGGCTCTTATCCGATACCTCTCCAGATTCCTGGATATTGATGATCTGGCT	970
Db	945	ATGCTCTCTTGTCCGATACCTTCCAGTGTGGCTGATGTTCCAAATTGATGCTGTA	1000
Qy	971	TGATGAGGATGCGTATGCGTGTGGAAATCAGATAACAAACTTGCAGTACCT	1031
Db	1005	TGATGAGGATGCGTATGCGTGTGGAAATCAGATAACAAACTTGCAGTACCT	1064
Qy	1031	ATCTCTATTGTTACTATGTTGCTGTTGACTGTGGATTGATGAGTGTGGCTCAGTTGGCT	1091
Db	1065	ACCTATATTGTTACTATGTTGCTGTTGACTGTGGCTGATGTTCCAAATTGATGCTGTA	1124
Qy	1091	TGCACTCTGATCAAGCAGCAACAGAGATGTTAATGCTGGCTTGGCT	1151
Db	1125	TGCACTCTGATCAAGCAGCAACAGAGATGTTAATGCTGGCTTGGCT	1184
Qy	1151	TGCAATCAACTAACCAAATACTCAGAGATGTTAGGAGAAAGTCAGGAGAGAG	1214
Db	1185	TAGCAATCAACTAACCAAATACTCAGAGATGTTAGGAGAACTTAACTGAGAG	1244
Qy	1211	TATACCTGCTCAAGATGATGAGCTGGGGCTCTGGAGACATATGCTG	1271
Db	1245	TCTCTTACCTCAAGATGAAATTAGCACATGAGGTTCTCGGAGTCAATGCTG	1300
Qy	1271	GAAGATGCTGAGCTGATGAGCTGGGGAACTTTAAGGAAACAAATTGAGGAGAAT	1333

DB 1305 GAAAGTGACGGATAATGGAGAACCTTATGAAAGCAATCCAGGGCAAGAAGT 1364  
 QY 1331 TCTTGTATGACTCAGAAAGGTGTCAGACRACTGACTCGACTGACTGCTGCT 1390  
 DB 1365 TCTTGTATGAGCAGGAAGGTGACAACTGAGCAGCAACTGAGCTGATGGCTGTAT 1424  
 QY . 1391 TAACAGCGCGCTGTATGCCAAGATATTGGCAGAGTTGAAAGCTAACAAA 1450  
 DB 1425 GGGCTCTTGCTGTGTAACGCCAGATACTGAGAGTCGAACCTGACTAACAA 1484  
 QY 1451 ACTTCACAAGGAGGGTTATGCAAGCAAGGCTCACCTGCCATTGCT 1510  
 DB 1485 ACTTCACAAGAGACCTTATGCAAAATCAGAAGCTAACCTTACCTATGCTA 1544  
 QY 1511 ATGCAAATTCCTTGCCCTTAATAGACT -TCTCTCAGCAAGACATGAATG 1569  
 DB 1545 ATGCAAATTCCTTGCCCTCAGACTCTGTCTCTCTAGCTTAAAGACTC 1604  
 QY 1570 AAGTAGTTGACTCAATG-----AGTATTATACTACTAAAGAAACTCAGGTACTG 1618  
 DB 1605 TCAGATTAAATTAAGCAAGAACATTCCTGTAAGAGATTATTAAAGTA 1664  
 QY 1619 TAATGAGATATCTTGTCTTGTAAATGTATCATCAAAGTAGATGT -TAATTCAATATG 1677  
 DB 1665 GATACTGGTSTATGATGTCACCTGATATCATCAAAGTAGTAAATTCATATA 1724  
 QY 1678 ACAATCTCTTGTAGATAT-TTCTCCAACTCATCAAAGTAGATGTAAAGTA 1727  
 DB 1725 ACAATCTTATGGTTGTATGTTACATCTTAAACCCTCGAGGAA 1775

**RESULT 4**  
 AAI66367 AAI66367 standard; cDNA; 1712 BP.  
 XX  
 AC AAI66367;  
 XX DT 29-JAN-2002 (first entry)  
 XX Nicotiana tabacum phytoene synthase coding sequence #2.  
 XX Phytoene synthase; zeta carotene desaturase; herbicide; transgenic plant;  
 KW plant growth regulator; herbicidal; tobacco; ss.  
 XX Nicotiana tabacum.  
 XX Key Location/Qualifiers  
 FH 333..1565  
 FT /\*tag\*<sup>a</sup>  
 FT /product= "phytoene synthase"  
 XX DE10022362-A1.  
 XX PD 15-NOV-2001.  
 XX PF 08-MAY-2000; 2000DE-1022362.  
 XX PR 08-MAY-2000; 2000DE-1022362.  
 XX PN (FARB ) BAYER AG.  
 XX Busch M, Hain R;  
 XX WPI; 2002-027336/04.  
 DR P-PSDB; AAM51842.  
 XX New nucleic acid encoding tobacco zeta-carotene desaturase, useful for  
 PT screening compounds with herbicidal activity -  
 XX PS Claim 14; Page 21-26; 44pp; German.  
 XX The present invention provides the protein and coding sequences of  
 CC phytoene synthases and zeta-carotene desaturase from Nicotiana tabacum.

CC The sequences can be used to identify compounds capable of altering the  
 CC expression of these genes, which are therefore useful as plant growth  
 CC regulators and herbicides. They can also be used to produce transgenic  
 CC plants. The present sequence is the coding sequence of a tobacco  
 CC phytoene synthase.  
 XX Sequence 1712 BP; 540 A; 265 C; 421 G; 475 T; 11 other;  
 SQ Query Match 49 6%; Score 857 8; DB 24; Length 1712;  
 Best Local Similarity 76.7%; Pred. No. 2.8e-24;  
 Matches 1206; Conservative 2; Mismatches 265; Indels 100; Gaps 9;  
 XX 132 GTGGATATCTCACAGTATTGGTAAATAGCTAGGTGAAAGCTAACATAA 191  
 QY 1328 GAGTAAATTATTAAATTTTATAAATTAAAGCAGGAAGGAAACAGAAAACGAA 277  
 Db 192 AGGAAGACAAAAACTGGGAATGGTTAGACACCAGGTTTCCTGTTCATGACAT 251  
 Db 278 AGTAAGACAAAAACCTGGATTGTTAGAAAGCCAAGGTTTCTGTTCAAA--AT 334  
 QY 252 GTCTGTGCTGTCTGGGTGTCTCCACACTCGAGGTCTCGATCAGGTGAGATT 311  
 Db 335 GTCTGTGCTGTATGGTTCTAC --CTTGTAAGCTCTCAATGGACAGATT 391  
 QY 312 GTTGATTCACTCCGAGAAACCGCTTTGATCAGCTCGTTCTCGAGA 371  
 Db 392 CTGGATTCACTCCGAGGAAACCGGTTTTCGTTGATTCGTCAGG -----CA 439  
 QY 372 TAGGATTGTATGTTGSAATGGGAACTAAAGGAGACAAAGGTGGAATTGG 431  
 Db 440 TAGGAATTAGTGTGCATAGAGAAACAGGGTGTGAAACAAAGGTGGAATTGG 499  
 QY 432 CTCTTAATTCGATCCAAGATTCATGTTGGTGGATCAAGAACACTGAAAGGAAAG 491  
 Db 500 ----- 499  
 QY 492 CACTTCCTGTCAGTCAGTCCAGTTGGCTAGGCCAGTGAGAAAT --GACTGTGTC 548  
 Db 500 -----TTCTGTAAGGTCATGCTGTTGGCTATGGTATGCTGAGATGAC 553  
 QY 549 ATCAGAAAAGGGTATGATGTTGTTAAGCAGCCTTACTGAAGGCGACT 608  
 Db 554 ATCAGAACATGGTTATGTTGTTAAACAGCTTGTGAGGCGATT 613  
 QY 609 GAGATTAACCTGATTTAGAGTGAAGCCGATATTGGTGTGTCAGCGAAATTGGCGCT 668  
 Db 614 GAGATCTGCTGATGATTAGAGTGAAGCCGAGATCCTCCCGGAAATTGACGTT 673  
 QY 669 GTTGAGTGAAGCATATGATCCTTGTGGCAAGATGATGTCAGTAAAGACATTTA 728  
 Db 674 GTTGAGTGAAGCATATGATGTTGAGTGAAGTGTGAACTGAGTATGCTGAGT 733  
 QY 729 CTTAGGAACCCAGCTATGACCCCCAGAGAGAACGCTATCTGGCCAATATGTGTG 788  
 Db 734 CTTHGAAACCATGTTATGACTCCAGAGAGAACGGCTATTGGSCAAATATGTGTG 793  
 QY 789 GTGAGAGAGAGGAGACGGCTTATGGCATACATAACTCCGCAAG 848  
 Db 794 GTGCAAGAGAGACAGTAACCTGATGTTGAGTGTGAACTTGGCCAAACGCTATGATGCT 853  
 QY 849 TTTRAGATAGCTGGAGACAGGCTGAAAGATATTTCAGTGGGGCCATTGATGATGCT 908  
 Db 854 CTTAGATAGCTGGCTTATGGCATACTGTCAGTGGCTGAGATTTCTGTGATGCT 913  
 QY 909 TGATGTTAGCTGGATGGTATGGCAAGATCAAACCTTCGATGCTGAGT 968  
 Db 914 CGATGCTGCTGCTGGCATACTGTCAGTGGCTTCAAGTCCAGTTGATGAGCT 973  
 QY 969 TATGATTGAAGGAATGGTATGGCAAGATCAAACCTTCGATGCTGAGT 1028  
 Db 974 TATGATTGAAGGAATGGTATGGCAAGATCAAACCTTCGATGAGCT 1033  
 QY 1029 ATATCCTATGTTACTATGTTGCTGTTACTGTGAGTTGATGAGTGGTCCAGTGTAGGG 1088



Qy	731	TAGGAACCAAGCTTAATGACAGAGAACAGAGCTATCAGGGCAATTATATGTGTGGT	790	AC	AAQ99323;
Db	766	TAGGAACCATCTATGACAGAGAACAGAGCTATCAGGGCAATTATGTGTGGT	825	XX	DT 13-APR-1996 (first entry)
Qy	791	GCAGGAGAACGGATGAGCTGTGATGCCCTAATGCACTCCACATAAACCGCAAGCTT	850	XX	DE Melon phytene-synthase gene.
Db	826	GCAGGAGAACGGATGAGCTGTGATGCCCTAATGCACTCCACATAAACCGCAAGCTT	885	XX	KW melon; phytene synthase; ripening; CDNA library; fruit; MEL5; tomato; RNA; probe; hybridization; polymerase chain reaction; PCR; antisense; transgenic plant; crop improvement; carotenoid; vector; ss.
Qy	851	TAGATGGTGGAGAACGGATGGGGATTTAGTGCGGCCATTTGATGCTGTGCTGTG	910	KW	KW -
Db	886	TAGATGGTGGAGAACGGATGGGGATTTAGTGCGGCCATTTGATGCTGTGCTGTG	945	KW	KW -
Qy	911	ATGCTGCTTTATCCGATACAGTCAGATTCCAGATTCCAGCATTCAAGATA	970	OS	Cucumis melo.
Db	946	ATGCTGCTTTATCCGATACAGTCAGATTCCAGCATTCAAGATA	1005	XX	W09602650-A2.
Qy	971	TGATGAAGGATGCTATGACTGTGAAATCCAGATACAAACCTTGATGAGCTAT	1030	PD	01-FEB-1996.
Db	1006	TGATGAAGGATGCTATGACTGTGAAATCCAGATACAAACCTTGATGAGCTT	1065	XX	06-JUL-1995; 95WO-GB01603.
Qy	1031	ATCTCPATGTTACTATGTTGCTGGACTGTGAGGTCTCGAGTTATGGTA	1090	XX	22-SEP-1994; 94GB-0019081.
Db	1066	ACCTCPATGTTATGACTGTGAGGTCTCGAGTTATGGTA	1125	PA	18-JUL-1994; 94GB-0014505.
Qy	1091	TGCACTTGATCAAGGACAACAAGAGTGTATAATGCTGCTTTAGGGC	1150	(ZENE ) ZENeca LTD.	
Db	1126	TGCACTTGATCAAGGACAACAAGAGTGTATAATGCTGCTTTAGGGAA	1185	PI	Grierson D, John I, Karvouni Z, Taylor J, Turner A;
Qy	1151	TGCAATCACTAACATAACTAGATGAGTAGGAGATGCCAGAGAAAGAG	1210	Watson C;	
Db	1186	TGCGGATCTCAACTAACGACATACUGGGATGTTGGAGAGATGCCAGAGAAAGAG	1245	XX	
Qy	1211	TATACPTGCCCTAAGATGTTAGCAAGGGGTCCTCGACAGAACATATTGCTG	1270	PS	Claim 2; Page 15-16; 22pp; English.
Db	1246	TCTACTTACCTCAAGTGAATTAGCAAGGGCACAAAGCTTCGAGCTTGTG	1305	XX	The sequence encodes melon phytene-synthase (MEL5 gene), and is almost full-length. The sequence has been isolated as a cDNA clone from a ripening-related cDNA library derived from climacteric melon fruit, using the tomato phytene-synthase cDNA (TOM5) as a heterologous probe. The MEL5 gene 5'-end has also been isolated by polymerase chain reaction and sequenced. The DNA may be used in sense or antisense constructs to modify gene expression in plants. The carotenoid content and related characteristics of plant parts (particularly fruit) may be modified in this way.
Qy	1271	GAAGAGTACTGATAATGGAGGAACTTATGAGAACAAATTGAGGGCGGAGAAAT	1330	CC	Sequence 1591 BP; 507 A; 237 C; 395 G; 452 T; 0 other;
Db	1306	GAAGAGTACTGATAATGGAGGAACTTATGAGAACAAATTGAGGGCGGAGAAAT	1365	CC	Query Match 49.1%; Score 847.6; DB 17; Length 1591;
Qy	1331	TCTTGTGATGACTCAGAAAGGTGTCACAGAACTGGACTCTGCTAGTAGATGCCCTGTG	1390	CC	Best Local Similarity 77.6%; Pred. No. 2.2e-231;
Db	1366	TCTTGTGATGACTCAGAAAGGTGTCACAGAACTGGACTCTGCTAGTAGATGCCCTGTG	1425	CC	Mismatches 0; Mismatches 249; Indels 79; Gaps 6;
Qy	1391	TAACAGCCCTGCTGTTGATGCCAGATATGGAGGATGAGCCAAAGCTCAACA	1450	CC	Query Match 101 TATAATCGTTGAAATTAGTGGATAGACTCTAGTGGATATCTAC--AAGTATGTTGTTT 157
Db	1426	GSGCATCTTGTGTTGATGCCAAATCTGGACGATGAGCTCAACA	1485	CC	DB 116 TAATTTGTTGAGTGGAAATATTCTCTAGTGGATCTACTAGGTAATTATTT 175
Qy	1451	ACTTCACAGGGGCTATGAGCAAGGCTTCTACCTTGCCATTGCTT	1510	CC	Qy 158 TGATAAAATAGCTGCTGAGTGGAGGTACATAAGGAAAGCAAACCTGGAAATGT 217
Db	1486	ACTTCACAGGGGCTATGAGCAAGGCTTCTACCTTGCCATTGCTT	1545	CC	DB 176 CTATAAAATAGCTGCTGAGTGGAGGTACATAAGGAAAGCAAACCTGGAAATGT 234
Qy	1511	ATGCAAAATCTCTGTCGCCCTTAATGAACT-TCTCTCCACTAGCAAGACATGAAATG	1569	CC	Qy 218 TTAGACCACCGGTTCTCTGTTCATGAGCATGTCCTGTTGGTTGGTT 277
Db	1546	ATGCAAAATCTCTGTCGCCCTTAATGAACT-TCTCTCCACTCTAACCTCTAACCTGCAAGCTAA	1605	CC	DB 235 TTAGACAAACCAAGT--TTCTCTGCTCAGATGTCCTGTTATGGTT 291
Qy	1570	AATAGTGTGCTAATGAAACTGACTGAAATGTTAAATGAAATCTCTAACCTGCAAGCTAA	1622	CC	Qy 278 CTCCCACTTCGAGGCTCTGCAATGGGACAGGATTGTCGGATTCACTGGAGAAACC 337
Db	1606	TGAGATTAATTAAGCAAGAAAGCATATTTACTATAAAAGAAATTCTAA	1665	CC	DB 292 CTC--CTTGTTGACTGCTCAATGGGAAAGTTCATGTCAGTCCGGAGGAACC 348
Qy	1633	TGAGATATCTT-----TGCTTAATGTTGATCATCAATGAGTTGATCTTAAATCAAT	1674	CC	Qy 338 GGCTTCTGATCATCCAGGTTCTAGTCGAGATAGAATTGATGGAAATGGAGAA 397
Db	1666	GTAAGATATGTTGATGTTGATGCTGTTGATCATCAAAAGTAGSTAGTAAATCCCAT	1725	CC	DB 349 GTTTTGTGATCATGAGG-----CATAGAATTGTTGCTCAGTCCAACTGAGCAA 396
Qy	1675	ATGACAAATCTCTGCTGAGAATTCTCCACACICATC	1713	CC	Qy 398 TCAAGAAAGGTGGAGACAAGGGAAATTGGCTCTTTAAATGCTGATCCAAAGATATT 457
Db	1726	ATPACAAATCTCTGATGTTGATGTCACAACTCTTAAGC	1764	XX	RESULT 6 AAQ99323 standard; cDNA: 1591 BP: XX

Db	397 TCAATAGGGT-----	407	Qy	1538 GAACTCCCTCCAACTAGCAAAGA 1561
Qy	458 CATGCTGGGGATAAAGACTGAAAGGGAAACTTCCTCGTACAGTCCAGTTTG 517		Db	1480 AACATGCCCTCTCTCAAAGATAAA 1503
Db	408 -----GGTGGAAAGCAACATTAATATGACGAATTCTGACGTTCTGCTATT 459			
Qy	518 TGGCTAACGCCAGCTGGAGAAATGACTGTCTCATAGAGAAAAGGTGTGGT 577			
Db	460 TGGFACTCCATCTGAGAACGGAGATGACATGGCTATGTGGTT 519			
Qy	578 TAAAGGAGGCAGCTTAGTGAAGGGAGCTGAGATCTACCGGAGATTAGAGT 637			
Db	520 TGAGGAGGCAGCCTGGTGAAGGGCAACTGACATGCTACCAATGAGAAGC 579			
Qy	638 CGGATATTGGTGGTGGGAATTTGGCTGTGAGTGGAGCATATGAGTCG 697			
Db	580 CGGATATACCTTATTCGGGGAAATTGGCTGTGAGTGGAGCATATGAGTCG 639			
Qy	698 AAGTAGTGGAGAGATGGAAAGACATTACTAGAACCTAATGACAGCTAAC 757			
Db	640 AAGTAGTGGAGAGATGGAAAGACATTACTAGAACCTAATGACAGCTAAC 699			
Qy	758 GAGAAGGGCTATCGGCAATATATGCTGGTGGAGGAACGGATGGCTTGTGATC 817			
Db	700 GAAGAAGGGCTATCGGCAATATATGATGGTGGAGAACAGATGAACTTGTGATC 759			
Qy	818 GCCCCPATGATCCACATRACTCGGCAATATGCTGGTGGAGAACGGCTGGAG 877			
Db	760 GCCCCAACGGCATCATPATATPACCCGGCACCTPAAGATGGTGGAAATATGGCTGAG 819			
Qy	878 ATATTCAGTGGGGCATTGATATGATGGTGTGCTGCTTATCGTACTGCTCCA 937			
Db	820 ATGTTTCAATGGGGCAATTGATCTGATGGTGTGCTGCTGAGTCAACGTTCA 879			
Qy	938 GATTTCCTGTGATATTCAGGATGATGTTGAGGGATGCTTATGGACTTGT 997			
Db	880 ACTTCCAGTGTGATATTCAGGATGATGCTGAGTGGATGCTGACTTGA 939			
Qy	998 GGAAATCCAGATAACACTTGTGAGTGGTGTGCTGAGTGGTGTGCTGAGTGG 1057			
Db	940 GAAATTCGAGATACACACTTCAGGATGATGCTGAGTGGTGTGCTGCTGCTG 999			
Qy	1058 CTGTAGATGTGATGGTGTGGTGTGGTGTGCTGAGTGGTGTGCTGAGTGG 1117			
Db	1000 CGGTGGGGTGTGATGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 1059			
Qy	1118 AGAGTGTATAATGCTGGCTGGTCAAGTCAACTAACCAATACTCTCA 1177			
Db	1060 AGAGCTTATAATGCTGGCTGGTGTGGATGCAAACTAACATACTACATACTCA 1119			
Qy	1178 GAGATGAGGAAGGAAAGGAGACTATACTGCTTCAAGGCAACAAAG 1127			
Db	1120 GAGATGTTGAGAAGGAGAGTGGCTAACAGTGAATTAGCAC 1179			
Qy	1238 AGGCAGGGCCTCCGACGAGACATATTCTGGAGAGTGTACTGATACTGGAGAAC 1297.			
Db	1180 AGGCAGGTCTCATCGATGAGATATTCTGGAGAGTGTACTGATACTGGAGAAC 1239			
Qy	1298 TTATGAGAACAAATTAGGGGAGGAATTCCTGAGTGTGAGTGTACTGGAGAAC 1357			
Db	1240 TTATGAGAACAAATTACATAGGGCAAGAAAGTCTTGTGAGGCAAGGCTGTA 1299			
Qy	1358 CAGAACTGACTCTGCTGATGGCTAACAGCGCTGTGTGTTATGCAAGA 1417			
Db	1300 CAGAACTGACTCTGCTGATGGCTAACAGCGCTGTGTGTTATGCAAGA 1359			
Qy	1418 TATTGGAGAGATGAGCCACGACTACACAACCTCAAGGGGGTATGTTGAGA 1477			
Db	1360 TACTAGATGAGATGAGCCACGACTACACAACCTCAAGGGGGTATGAGA 1419			
Qy	1478 AGCCAAAGAAGCTTCACCTGGCCATTCTATGCAAATACTCTTGTGCCCCCTAATA 1537			
Db	1420 AATCAAAGAAGTGTGATGCAATCATGCAAATACTCTGCCCCCTAACAA 1479			
Qy	1538 GAACTCCCTCCAACTAGCAAAGA 1561			
Db	1480 AACATGCCCTCTCTCAAAGATAAA 1503			
	RESULT 7			
	AAQ12495 standard; cDNA: 1646 BP.			
	XX ID AAQ12495			
	AC AC AAQ12495;			
	XX DT 18-SEP-1991 (first entry)			
	XX DE Tomato fruit ripening related gene pTOM5.			
	XX KW ripening; lycopene; transgenic tomato; ss.			
	XX OS Lycopersicon esculentum var. Ailsa Craig.			
	XX FH Key CDS			
	XX FT FT			
	XX /*tag= a.			
	XX Location/Qualifiers			
	XX 201.1436			
	XX WO9109128-A.			
	XX PD 27-JUN-1991.			
	XX XX PP 10-DEC-1990; 90WO-GB01924.			
	XX XX PR 13-DEC-1999; 89GB-0028179.			
	XX XX PA (ICIL ) IMPERIAL CHEM IND'S PLC.			
	XX PI Bird CR, Grierson D, Schuch W;			
	XX XX DR WPI; 1991-208154/28.			
	XX XX PS Disclosure: Fig 1; 35pp; English.			
	XX CC Clone pTOM5 was derived from a cDNA library isolated from ripe			
	CC tomato RNA (Slater et al., Plant Molecular Biology 5, 137-147, 1985). The protein it encodes is estimated to have mol. wt. ca.			
	CC 48KD. pTOM5 is expressed in ripening fruit. Strongest expression is at the full orange stage of ripening; no expression is detected in green fruit. See also AAQ12494.			
	XX SQ Sequence 1646 BP; 529 A; 249 C; 387 G; 481 T; 0 other;			
	Query Match 48.6%; Score 840.4%; DB 12; Length 1646;			
	Best Local Similarity 74.3%; Pred. No. 2.5e-29; Mismatches 331; Indels 92; Gaps 9;			
	Matches 1221; Conservative 0; Mismatches 331; Indels 92; Gaps 9;			
Qy	101 TATAATCGTGTGAAATTAGTGGATAGACTCTAGTGGATATCT--AAGTATTGGTTTT 157			
Db	53 TAATTTGTTGAGTGGAAATATCTCTAGTGGAAATCTAGTGGATTAATTATTT 112			
Qy	158 TGATAAAATAGGTGTAGGTGAGGTGAGGTTAAATAAGGAAAGACAAAAAAACTTGGAAATTGT 217			
Db	113 CTATTAACATAGTAAGTGGAAAGGTGACA -AAAGAAAGACAAAAAAATCTGGAAATTCT 113			
Qy	218 TTAGGACCCAGGTTCTGGCTGATGGCTGTTCTGTTGAGTGGCTGTTCTGTTGCTGCTGTT 277			
Db	172 TTAGGACCAACAAAGT -TTTCCTGCTCTGAAATGCTGTTCTGCTGTT 228			
Qy	278 CTCCCACTTCGGAGGCTCGAATGGCTCAGGAGATTGTTGGATTCTGCGAGAAGGAACC 337			
Db	229 CTC - CTTGTGACCTCTCAGATGGCAACATGGTTCATGAAATCATGGCAATGGTTCATG 285			



CC and other carotenoids have been used as food colours, animal feeds and in the pharmaceutical and cosmetics industries.

XX Sequence 1316 BP; 403 A; 221 C; 342 G; 350 T; 0 other

SQ Query Match 46.9%; score 811.2; DB 19; Length 1316;

Best Local Similarity 80.2%; Pred. No. 4.9e-221;

Matches 1039; Conservative 0; Mismatches 173; Indels 84; Gaps 4;

250 ATGTCGTGTCCTTGTGGTGTCTTCCCACTTCGGAGGTCGATGGACAGGA 309

Db 1 ATGTCGTGTCCTTGTGGTGTCTTCCCACTTCGGAGGTCGATGGACAGGA 57

310 TTGTGGATTCAGTCGAGAAAGGAAACCGCGTCCTTGTATCATCAGGTTCTPAGCTCGA 369

Db 58 TTCTGGATTCATACTGGGGAAACCGGGTTTTGATGGTGAGG----- 105

QY 370 GATAGGAATTGATGTGGATGGAGAACAGAAGGGGGAGACAANGGTGAATT 429

Db 106 CATAGGAATTGATGTGGATGGAGAACAGAAGGGGTGGACAAATGTGGAAATT 165

QY 430 GGCTCTTAATTGTGTGATCCAAGATTATGCTGGGGATGAAAGGGA 489

Db 166 GGTTCTGTAA----- 175

QY 490 AGCACTTTCTCTGTACAGTCAGCTGGCTAGCCCAGCTGGAAAT---GACTGNG 546

Db 176 -----AGCTGTGATGGGGTACACGGGGAAATGGGACAGATG 219

QY 547 TCATAGAGAAAAAGGTGGATGTGGATTAAAGCAGGCACTTATGTGAGGGAG 606

Db 220 ACATGAAAGCATGGTTATGATGCTGGATTGATGAGGGAG 279

QY 607 CTGAGATCTACCGATGATTAAGTGAAGCCGATATTGTGTTCCAGGGAAATTGGCC 666

Db 280 TTGAGATCTACTGATGATTAAGTGAAGCCGAGATECCTCTCCGGGAATTGAGC 339

QY 667 TTGTGAGTGAAGCATGATGATGCTGGCAACTATGTGAGGTATCRAAGACATT 726

Db 340 TTGTGAGTGAAGCATGATGATGCTGGCAACTATGTGAGGTATCRAAGACATT 399

QY 727 TACTTGAACCAACCTATAATGACCCCCAGAGAGGCTATCTGGCAATAATATG 786

Db 400 TACTTGAACCTATAATGACCCCCAGAGAGGCTATCTGGCAATAATATG 459

QY 787 TGGTSCAGGGAACGGATAAGCTGTTGTTGCGCTTAATGATCCACATTAACCTCGGA 816

Db 460 TGGTSCAGGGAACGACRACGACRACGACRACGACRACGACRACGACRAC 519

QY 847 GCTTGTAGATAGTGGAGGACAGCTGGAGATATTGTGTTGGGCCATTGTGATG 906

Db 520 GCCTTAGATGGTGGAAACCGCTGGAGAAGTTCAGTGGCGGCCATTGACAG 579

QY 907 CTGATGTCGCTTTATCGGATACGTGTCAGATTTCCTGTGATATTGAGCT 966

Db 580 CTCGATGCTGCTTGTCCGATACGTTCAAGTGTGATATTGAGCTTCAG 639

QY 967 GATATGATGAAAGGAATGGGTATGGCTGGAATCCAGATAAACCTTGATGAG 1026

Db 640 GATATGATGCAAGGATGGGTATGACATGAGGAGTCAGATACGAACTTGATG 699

QY 1027 CTATATCTPATGTTACATGTTGCTGGTACGTGGATTGATGAGTTCCAGTTG 1086

Db 700 CTATACCTATATGTTACGTGTTGCTGGTACAGTTGGGTGAGGTTCAATTAG 759

QY 1087 GGTATTGCACTGTGATCAAGGCAACAGAGAGTCTATAATGCTGCTTGGCTTA 1146

Db 760 GGCATGCGACTGTGATCAAGGCAACAGAGTGTGATATGACGTTGGCTTG 819

QY 1147 GGGCTTGCAAAATCAACTAACTAACCTAACTAACCTAACATGAGATGAGG 1206

Db 820 GGTATCGGGATCACTAACCTAACATCAGATGCGGAGAAGATGCCAGAGGG 879

CC	QY	1207 AGAGTATACTTGCCTCAAGATGAATTAGCACGGAGGGCTCTCCGACGAACTATT 1266
XX	Db	880 AGAGTCTACTTACCTCAAGATGAATTAGCACGGAGGTCTCTCCGACGATATT 939
SQ	QY	1267 GCTGGAAAGTGTGACTGATAATGGGAAACTTTATGAAGAAACAAATTCAAGGGCGAGG 1326
Query Match 46.9%; score 811.2; DB 19; Length 1316;	Db	940 ACTGGAAAATGTGACTGATAATGGGAAAGCTTATGAAGGAACTTCAGGGAAAGA 999
Best Local Similarity 80.2%; Pred. No. 4.9e-221;	QY	1327 AAATCTTCTGATGACTGAGGAAAGGTGACAGAATCTGCTACTGATGGCT 1386
Matches 1039; Conservative 0; Mismatches 173; Indels 84; Gaps 4;	Db	1000 AAGTCTTCTATGAGGCAAGGAGTACACACTGAGCTGAGCTAGATGGCT 1059
250 ATGTCGTGTCCTTGTGGTGTCTTCCCACTTCGGAGGTCGATGGACAGGA 309	QY	1387 GTGTTAACAGCGCTGCTGTGATGCAAGATATTGGACAGGATGAAAGCCAAACGACTAC 1446
1 ATGTCGTGTCCTTGTGGTGTCTTCCCACTTCGGAGGTCGATGGACAGGA 57	Db	1060 GTATGGCATCTTCTGTGTTGACGCCAATACTGACGGAGATGAGGCTAATGACTAC 1119
310 TTGTGGATTCAGTCGAGAAAGGAAACCGCGTCCTTGTATCATCAGGTTCTPAGCTCGA 369	QY	1447 AACACTTCAAGAGGGTTATGAGGCTCTACCTGGCCATT 1506
58 TTCTGGATTCATACTGGGGAAACCGGGTTTTGATGGTGAGG----- 105	Db	1120 AACACTTCAAAAGAGGCTTATGTGAGCAAATAAAGAGCTAAATTCCTTACACTATT 1179
370 GATAGGAATTGATGTGGATGGAGAACAGAAGGGGGAGACAANGGTGAATT 429	QY	1507 GCTTATGCAAAATCUCITGTCGCCCCCTAAATAGAACCT 1542
106 CATAGGAATTGATGTGGATGGAGAACAGAAGGGTGGACAAATGTGGAAATT 165	Db	1180 GCTTATGCAAAATCTCTGTGCCCCCTACAGAACCT 1215
QY 430 GGCTCTTAATTGTGTGATCCAAGATTATGCTGGGGATGAAAGGGA 489	RESULT 9	
Db 166 GGTTCTGTAA----- 175	ID	AAZ99482 standard; cDNA; 1239 BP.
QY 490 AGCACTTTCTCTGTACAGTCAGCTGGCTAGCCCAGCTGGAAAT---GACTGNG 546	AC	AAZ99482;
Db 176 -----AGCTGTGATGGGGTACACGGGGAAATGGGACAGATG 219	XX	
QY 547 TCATAGAGAAAAAGGTGGATGTGGATTAAAGCAGGCACTTATGTGAGGGAG 606	XX	03-JUL-2000 (first entry)
Db 220 ACATGAAAGCATGGTTATGATGCTGGTTATGATGAGGGAG 279	XX	XX
QY 607 CTGAGATCTACCGATGATTAAGTGAAGCCGATATTGTGTTCCAGGGAAATTGGCC 666	DE	DE
Db 280 TTGAGATCTACTGATGATTAAGTGAAGCCGAGATECCTCTCCGGGAATTGAGC 339	XX	XX
QY 667 TTGTGAGTGAAGCATGATGATGCTGGCAACTATGTGAGGTATCRAAGACATT 726	KW	Gibberellic acid; copaly diphosphate synthase; 3beta-hydroxylase;
Db 340 TTGTGAGTGAAGCATGATGATGCTGGCAACTATGTGAGGTATCRAAGACATT 399	KW	2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta hydroxylase;
QY 727 TACTTGAACCAACCTATAATGACCCCCAGAGAGGCTATCTGGCAATAATATG 786	KW	seed germination; seedling growth; gibberellin biosynthetic pathway;
Db 400 TACTTGAACCTATAATGACCCCCAGAGAGGCTATCTGGCAATAATATG 459	KW	transgenic plant; hypocotyl; spicotyol; ssp.
QY 787 TGGTSCAGGGAACGGATAAGCTGTTGTTGCGCTTAATGATCCACATTAACCTCGGA 816	OS	Lycopersicon esculentum.
Db 460 TGGTSCAGGGAACGACRACGACRACGACRACGACRACGACRAC 519	OS	
QY 847 GCTTGTAGATAGTGGAGGACAGCTGGAGATATTGTGTTGGGCCATTGTGATG 906	XX	Location/Qualifiers
Db 520 GCCTTAGATGGTGGAAACCGCTGGAGAAGTTCAGTGGCGGCCATTGACAG 579	PH	1..1239
QY 907 CTGATGTCGCTTTATCGGATACGTGTCAGATTTCCTGTGATATTGAGCT 966	FT	/tag= "phytoene synthase"
Db 580 CTCGATGCTGCTTGTGCCGATACGTTCAAGTGTGATATTGAGCTTCAG 639	FT	/transl_except= (pos: 1027..1029, aa: Lys)
QY 967 GATATGATGAAAGGAATGGGTATGGCTGGAATCCAGATAAACCTTGATGAG 1026	FT	/transl_except= (pos: 1057..1059, aa: Arg)
Db 640 GATATGATGCAAGGATGGGTATGACATGAGGAGTCAGTTCAAGTGTGATG 699	XX	XX
QY 1027 CTATATCTPATGTTACATGTTGCTGGTACGTGGATTGATGAGTTCCAGTTG 1086	PN	WO200009722-A2.
Db 700 CTATACCTATGTTACGTGTTGCTGGTACAGTTGGGTGAGGTTCAATTAG 759	XX	
QY 1087 GGTATTGCACTGTGATCAAGGCAACAGAGAGTCTATAATGCTGCTTGGCTTA 1146	PD	24 -PEB-2000.
Db 760 GGCATGCGACTGTGATCAAGGCAACAGAGTGTGATATTGACGTTGGCTTG 819	XX	XX
QY 1147 GGGCTTGCAAAATCAACTAACCTAACTAACCTAACATGAGATGAGGAGA 1206	PP	10-AUG-1999; 99WO-US18066.
Db 820 GGTATCGGGATCACTAACCTAACATCAGATGCGGAGAAGATGCCAGAGGG 879	XX	PR 10-AUG-1998; 98US-0096111.
CC	PI	07-JUN-1999; 99US-0137977.
CC	PA	(MONS ) MONSANTO CO.
CC	DR	WPI: 2000-224351/19.
CC	DR	P-PSDB: AAY84101.
Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone	PT	
Claim 45; Page 254-255; 267pp; English.	PT	
CC	PS	
The present sequence encodes a phytoene synthase polypeptide, which	CC	



The present sequence encodes phytoene synthase 4. It was isolated from a cDNA library prepared from mRNA extracted from the petals of Gentiana lutea. The nucleic acid sequence was amplified from the library using PCR primers AAV16959-53. The phytoene synthase gene is useful for breeding plants with variable flower colours.

Sequence 2868 BP; 887 A; 499 C; 648 G; 833 T; 1 other;

Query Match 40.1%; Score 692.4; DB 19; Length 2868;  
Best Local Similarity 73.6%; Pred. No. 6e-187;  
Matches 949; Conservative 0; Mismatches 311; Indels 30; Gaps 4;

Qy 240 TTTCATGAGCATGTGTCTTTCCTCCACTTCCGAGGTCTCGAA 299  
Db 390 TTCTGTAAATGCTATGTAGCTTGTAGCTTAGGGTTGCCGTTGA 449

Qy 300 TGGGACGATTGTTGGATCTAGTCGAGBAGGAAACCCTGCCTTGTCACTCCAGGT 359  
Db 450 TGGCATGTCTTCGGAGCAATTGAGAACAGTACCTTTTTCG----- 495

Qy 360 CCTASOTCGAGATGAGAATTGAGATGGTGGAGAATCAGAAGAGTGGGAGACAG 419  
Db 496 -----GATAAAAGTTTAATGTCAGATGGAGAAGTACCTTTTTCG----- 545

Qy 420 GTGGATTGTTGGCTTTAATGCTGATCAAGATATTGATGTTGGGGATCAAAGAC 479  
Db 546 GCGTGATCACGTTATGGGTGGCATGTTGAGTTGAGTTGAGTCGGAT 605

Qy 480 TGAAA---AGGAACCACTTCTCTGTCAGTTGGCTGAGCTGGGAGA 536  
Db 606 AGAGACCCGGAGAAAGATTATCGTAACTCCAGTATATAGCTCCAGGA 665

Qy 537 AATGACTGTTCATGAGAAAAGGGTGTATGAGTGGATTAAAGCAGCCAGTTTGT 536  
Db 666 ATAGGAGTACATGAGCAAAGCTTATGATGTCGTTAAAGCAGCAGCTTGT 725

Qy 597 GAAGGGCACTGTGAGATCPACCGATGATTAGATGAGTGAACCCGATAATTGTGTTCCAG 656  
Db 726 TAATGACACTTGGGTCPAGAGAAATTGGGTGAGAACCGACATTTGGCCAG 785

Qy 657 GAATTGGGCTTGTGAGCTGAGCATATGACCTGTTGGCAAGTATGTGAGATTC 716  
Db 786 AACACGCAAGCTGTGAAATGAGCTTATGTCAGAAATATGGCTGATATG 845

Qy 717 AAAGACATTTACTTAAAGAACGCTATGACCCAGAGAACGAGAACGCTTCTGGC 776  
Db 846 CAAGCTATTTACTTGGGACCCAGCTCATGACCCGGAGGGTTACCTGGCC 905

Qy 777 ATATATGTGTGGTCAGGAGAACGGATGAGCTGTTGTTGGCCCTAATGCACT 836  
Db 906 GATATATGTATGGCTATGTCAGGAGAACGATGAGCTGTTGTTGGCCCTAATGCACT 965

Qy 837 AACCTCGCAAGCTTATGATAGGTGGAGGACCAAGCTGGAGATATTTCAGTGGGGCC 896  
Db 966 AAATCCAAACGGGTATGATAGGTGGAAACCAAGATTAGAGATGTTAAAGGCCAAC 1025

Qy 897 ATTGTATGCTTGTGATGTCAGTATGTCAGGATGGCTATGCTGTTGGAAATCCAGATACAAC 1016  
Db 1026 TTTCATGATGCTTGTGCTTATGTCAGGATTTGGCTATGTCAGGATACAAC 1085

Qy 957 GGCATTCAGAGATATGATGAGGAGATGGCTATGCTGTTGGAAATCCAGATACAAC 1085  
Db 1086 GCCATTAGGATGATGAGGAGATGGCTATGCTGTTGGAAATCCAGATACAAC 1145

Qy 1017 TTTCATGATGCTTATGTCAGTATGTCAGGATTTGGCTATGTCAGGAT 1076  
Db 1146 TTTCATGATGCTTGTGCTTATGTCAGGATTTGGCTATGTCAGGAT 1205  
Qy 1077 TCCAGATTTGGGTATGCTGCTTATGTCAGGATTTGGCTATGTCAGGAT 1136  
Db 1206 ACCAGTAACTGGCATGCTGACCTGAAAGTGTATGTCAGGAT 1265  
Qy 1137 TTGGCTTAGGCTTGGGATGAGATGTCAGGATATACTCAACAAATCAAC 1196

Db 1266 TTATCTTGGGATGCAACCTGACTAACATTCTPAAAGGGTGTGAGAGATGC 1325  
Qy 1197 CAGAAGGAAGAGTATACTGGCTCAAGTGAATAGCACAGGAGGGCTCTCGAGCA 1256  
Db 1326 AAGRAGGGAGAGTGTACCTCAAGTGAATAGCAACAGGAGTTATCGATGA 1385  
Qy 1257 AGATATTTGCTGGAGAGTGTACAGAAAGTGTACAGAAAGTGTACAGTAA 1445  
Db 1386 GGACATTGTTGCTGGAAAGTTAGACAAATGGGGATTTTATGAGAGCAATCAA 1433  
Qy 1317 GAGGGGAGAAATTCTTGTGACTGAGTGGACTCTGC-TA 1375  
Db 1446 AAGGGCTAGAAATCTATGATGATGTCAGGAAAGGACTCCGAACTCAGTC 1505  
Qy 1376 GTAGATGGCCCTGTTAAC--AGCCCTGCTGTTGATCGCAAGATAATTGGACGAGATTGA 1433  
Db 1506 GCAGATGTCGTTGGCCAGGTGTTGCTTTATGAAAAATTGGATGAAATGAGA 1565  
Qy 1434 AGCCAACGACTACACAACTTCACAGGGCTPATGTAACAAAAGGCAACTCTCT 1493  
Db 1566 AGCARATGACTACARAACTTCACRAAAAGGCTPATGTAACAGGCAAAAGA 1625  
Qy 1494 CACCTTGCCCCATTGGGCTPATGTAACAAAATGCAAAATCTCT 1523  
Db 1626 AGCTATGCTGTCAGTGTGCCCAGCTCTCT 1655

RESULT 11

AAV16949 standard; cDNA to mRNA; 1921 BP.

XX ID AAV16949

XX DT 06-JUL-1998 (first entry)

XX DE Nucleic acid encoding phytoene synthase 2.

XX KW Phytoene synthase; breeding; variable flower colour; ds.

XX OS Gentiana lutea.

XX FH Key

XX FT CDS

XX Location/Qualifiers

412\_1689

XX FT

XX PN

XX JP10084966-A.

XX XX

XX PD 07-APR-1998.

XX XX

XX PF 17-SEP-1996;

XX DR 96JP-0245107.

XX PR 17-SEP-1996;

XX DR 96JP-0245107.

XX PA (IWAT-) IWATE KEN.

XX XX

XX WPI; 1998\_264853/24.

XX DR P-PSDB; AAW46952.

XX PT Phytoene synthase gene - useful for breeding plant of variable flower colour

XX XX

XX PS Claim 2; Pages 7-9; 15pp; Japanese.

XX CC The present sequence encodes phytoene synthase 2. It was isolated from a cDNA library prepared from mRNA extracted from the petals of Gentiana lutea. The nucleic acid sequence was amplified from the library using PCR primers AAV16952-53. The phytoene synthase gene is useful for breeding plants with variable flower colours.

XX SQ Sequence 1921 BP; 633 A; 296 C; 438 G; 554 T; 0 other;

XX Query Match

39.3%; Score 678.4; DB 19; Length 1921;

Best Local Similarity Matches 934; Conservative 0; Mismatches 326; Indels 30; Gaps 3;	Db 1398 TGAGGACATTTGGCTGAAAGTACAGACAAATGGAGGATTATGAGAACAAAT 1457
QY 240 TTTCATGACATGTCGTGTTGGCTTCTCCACTTCGGGTCCTCGAA 299	Qy 1314 TCAGAGGGCAGGAATCTTGATGATGTCAGAGAAGGTGTCACAGACACTGGACTCTGC 1373
Db 402 TCTCTGTTAACATGTCATTGCTTACGCTATGGTGTGCGAATGTTGAG 461	Db 1458 CAAAGGGCTAGAAATCTCATGATGTCAGAAAGTCCCAGACTCGTCGC 1517
Qy 300 TGGACAGGATGTTGGATTCAGTCAGTCAGGAGGAAACCGCTCTTGATCATCAGGTT 359	Qy 1374 TAGTATGGCTGTAAACAGCTGCTGTTATGCAAGATATGGAGGATGAA 1433
Db 462 TGGCAATGTTCTGGCAATTGATGAAAGTACCATTTTCG----- 507	Db 1518 GAGCAGATGGCTGTGTCGGCAGCGTCTTATGAAAATATGGATGAGATA 1577
Qy 360 CCTAGCTGAGATGGGATATGGAAATCAGAAAGTGGGAGACAAG 419	Qy 1434 AGCAACGACTACACACTCACAAAGGGCTTATGTTAGCAAGGCCAAAG 1493
Db 508 -----GTTAAAGTTTAATGPAACATGGAGGTTAGAAAGTAGACCAAAG 557	Db 1578 AGCAAAATGACTACACATTACACAAAGGGCTTATGTTAGCAAGGCCAAAG 1637
Qy 420 GTGGAATTGGCTCTTAATGCTGATCCAAAGATATTCAATGCTGGGGATCAAGAAC 479	Qy 1494 CACCTGGCCCAATTGCTTATGCAAAATCT 1523
Db 558 GGCTAGTACACCTTATTGGGTTGGAGATTTAGTCAATGGCTGTTGATT 617	.Db 1638 AGCTATGCTGTAGATGTGCAAGTCT 1667
Qy 480 TGTAA----AGGAAGCACTTCTCTGACAGTCAGTCCAGT - TTGGGGCTAGCCAGCTGG 533	RESULT 12
Db 618 AGAACCCCCGGAAAGAAGATATCGTATCCTCCAGTAAATAGCTACCCGGCAG 677	AAV16948 ID: AAV16948 standard; cDNA to mRNA; 2085 BP.
Qy 534 AGAAATGACTGTTGTCATCAGAAALAGGTGTATGTTAAAGCAGGACCTT 593	XX
Db 678 GAGAATGAGGTGACTCAGCAAAGTTATGTTAAAGCAGGACCTT 737	XX DE Nucleic acid encoding phytoene synthase 1.
Qy 594 AGTGAAGGGCAGCTGAGATCTACCGATGATTAGAAGTGAAGCCGGATATTGGTGTCC 653	XX DE phytoene synthase; breeding; variable flower colour; ds.
Db 738 GATTAATGACAGTTGAGTCATGAGGAAATTGGAGGTAAACCGACAAATTITGCC 797	XX KW
Qy 654 AGGGAATTGGCTCTGTTGAGTAAAGCATATGATGTTGTCAGGAGATA 713	XX Gentiana lutea.
Db 798 AGGAAACCGGACGTGTTGAATGAACTGATGTTGAGGATGTGTTGAAATA 857	OS
Qy 714 TGCAAACACATTACTGAGAACCTATGTTGAGGAAATGTTGAGCTATG 773	XX
Db 858 TGCCAAGTCATCCTACTGGGAAACCAGCTCATGACACCGCTCATGAC 917	XX
Qy 774 GCGAAATATGTTGTCGGTCAAGGATGTTGAGCTTGTGTCAGGAGATA 833	PD 07-APR-1998.
Db 918 GGGGATATATGTTGTTGAGGAGCTATGTTGAGGAGCTTGTGTCAGG 977	XX 07-SEP-1996; 96JP-0245107.
Qy 834 CATAACCTCGCAAGCTTAACTGATGTTGAGGAGCTATGTTGAGGAGCTTGTGTCAGG 893	XX 07-SEP-1996; 96JP-0245107.
Db 978 CATAAACTCAACCGGTTAGTAGGGAGCAAGATAGAGATGTTCAACGGCA 1037	PA (IWATE KEN.
Qy 894 GCCATTGATATGCTTGTGCTTATCGATGTTGTCAGTTGTCAGTGTGAT 953	XX WPI: 1998-264853/24.
Db 1038 ACCCTTGTGATGCTGCTGATGTTGATCCTGATACCATTTGAGGACAT 1097	DR P-PSDB; AAW46961.
Qy 954 TCAAGCAATTGAGATGATGAGGAAATGGTATGACTGTTGAAATCGATAAA 1013	XX Phytoene synthase gene - useful for breeding plant of variable flower colour
Db 1098 CCAGCCATTGAGATGATGAGGAAATGGTATGAGGAAATGGTATGAGATAAA 1157	XX Claim 1; Pages 5-7; 15pp; Japanese.
Qy 1014 AACCTTCGATGAGCTATATCTTATGTTCTACTGTTGTCAGTGTGAG 1073	XX
Db 1158 GAATTCTGATGGCTGATCTTACTGTTATGGCTGATGTTGAGGAGAA 1217	CC The present sequence encodes phytoene synthase 1. It was isolated from a cDNA library prepared from mRNA extracted from the petals of Gentiana lutea. The nucleic acid sequence was amplified from the library using PCR primers AAV16952-3. The phytoene synthase gene is useful for breeding plants with variable flower colours.
Qy 1074 TGTTCAGTTGGATTGGATATGACCTGAAATCAAGAGTGTATATGG 1133	CC
Db 1218 TGTACCAAGTAATGGCATGTCATGTTGATCCTGATACCATTTGAGGACAT 1277	CC
Qy 1114 TGTCTGGCTTGTAGGGCTTGTGAAATCAACTAACATAACTCAGAGATGTTGAG 1193	CC
Db 1278 AGCTTTATCTTGGGATGCGAACCTGGCTGACTAACATCTAAGGATGTTGAGAA 1337	CC
Qy 1194 TGGCAGAGAGGAAAGGATATACTGGCTCAAGTGAATTTGACAGCAGGCTCTCGCA 1253	CC
Db 1338 TGGAAAGAGGAAAGTGTACCTACCAAGTGAATAGCAAGCAGTTTAICAGA 1397	CC
Qy 1254 CGAAGACATATTGCTGGAGGAGTGTACGTTAGGAACTTATGAGAAACAAAT 1313	CC
	SQ Sequence 2085 BP; 654 A; 320 C; 479 G; 632 T; 0 other:
	Query Match Score 38.8%; Length 2085;
	Best Local Similarity 72.0%; Pred. No. 9.8e-181;
	Matches 929; Conservative 0; Mismatches 331; Indels 30; Gaps 3;
	Qy 240 TTTCATGAGCTCTGTTGCTTCTCCCACTCCGAGGTCTCGAA 299
	Db 576 TCTCTGTTAACATGCTTATTTGAGCTGATGGGTGTCAGTTGAGTTGAG 635
	Qy 300 TGGGACAGGATGTGGTGGATGCTGAGGAAACCGGTCTCAGCTCAGGTT 359



Qy	480	TGAA---AGGAAGGCACTTTCCTGTACAGTCAGTCCAGTTGGCTAGCCAGCTGGAGA	536		RESULT 14	
Db	705	AGAACCCGGAAAGAAGATPATCGTATCCCTCCAGATTATAGCTACCCGGCAGAGA	764	AAC35120 ID XX	AAC35120 standard; DNA; 1703 BP.	
Qy	537	AATGACTCTGTCATCAGAAAAGGTGATGTTGTTAAACGCCAGCTTGT	596	AC XX	AAC35120;	
Db	765	AATGACGATGACATCAGCAAAAGTTATGATGTTAAACGCCAGCTTGT	824	XX DT	17-OCT-2000 (first entry)	
Qy	597	GAAAGGGAGCTGAGATCTACCGATGATTAAAGTGAAGCCGATATGTTGTCAGG	656	DE XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 9067.	
Db	825	TAATAGACAGTGGGCTAGAAAATTGGGGTAACCGACATATTGTCAGG	884	KW XX	Hybridisation assay; genetic mapping; gene expression control;	
Qy	657	GAATTGGCTGTTGAGCATATGACGTTGGCAAATATGCAAGATATGC	716	KW XX	protein identification; signal pathway; signal transduction pathway;	
Db	815	AACCGCAACGCTGTTGATGAGCTATGATGGTCAATATATGC	944	KW XX	metabolic pathway; promoter; termination sequence; ss.	
Qy	717	AAGACATTTACTTAGAACAGATAATGACAGAGATCTGGC	776	OS XX	Arabidopsis thaliana.	
Db	945	CAAGTCATCTACTGGGAAACCCAGCTATGACACCGGAGGGTTAGTATCTGGC	1004	PN XX	EP1033405-A2.	
Qy	777	AATATATGTTGTTGAGGAGACGGATGAGCTTGGATGCCCTTAATGCCACAT	836	PD XX	06-SEP-2000.	
Db	1005	GATATATGTTGTTGAGGAGACAGATGTTGATGCCCTAACGCTCAATA	1064	PF XX	25-FEB-2000; 2000EP-0301439.	
Qy	837	AACCTCCGAAGCTTAGATAGTGGGAGACAGGCTGGAGATAATTCTAGTGGGGCCC	896	PR XX	25-FEB-1999; 990US-0121825;	
Db	1065	AAATCCACCGCCTTAGATAGTGGGAGCAGATTAGAAAGTGTTCAAAGGGCAACC	1124	PR 05-MAR-1999; 990US-0123180;		
Qy	897	ATTGATATGCTGTATGGCTGTTATCGAAGATTCCTGTGATATTCA	956	PR 09-MAR-1999; 990US-0123548.		
Db	1125	TITTGATATGCTGTATGGCTTAACTGATACCAAGTATCTGGGACATCA	1184	PR 23-MAR-1999; 990US-0125788.		
Qy	957	GCCATTGAGATGATATGATGAGGAATGCTGATGGACTTGTGAAATCAGATAACAAAC	1016	PR 25-MAR-1999; 990US-0126264.		
Db	1185	GCCATTGAGATGATGAGGAATGCTGAGAAATCAGATAACAA	1244	PR 29-MAR-1999; 990US-0126785.		
Qy	1017	TTCGATGAGCTATATCTCTATGTTACTATGTTGCTGTACTGTAGATGATGTT	1076	PR 01-APR-1999; 990US-0127462.		
Db	1245	TTCGATGAGCTATCTCTATGTTACTGTATATGCTGTACTGTAGATGATGATG	1304	PR 06-APR-1999; 990US-0128234.		
Qy	1077	TCCAGTTGGTATTCACCTGAAATCAAGCCAACACAAGAGGTATAATCTGC	1136	PR 08-APR-1999; 990US-0128714.		
Db	1305	ACCAGTATGGGATTSCACCTGAAATCAAGCCAACACAAGTGTATAATCGAGC	1364	PR 10-APR-1999; 990US-0129845.		
Qy	1137	TTCGGCTTGGCTTCAACTAACAATACCAATTACTCAGAGTGTAGGAAGATGC	1196	PR 14-APR-1999; 990US-0130077.		
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Qy	1197	CAGAAGGAAAGGATATGATCTCTCAAGATGAATTAGCACAGGAGGCCTCTCGGACGA	1256	PR 23-APR-1999; 990US-0130510.		
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Qy	1257	AGACATTTGCTGGAGAGTGAATGAGCTATGAGAAACATTATGAGAAACATTCA	1316	PR 28-APR-1999; 990US-0131449.		
Db	1485	GGACATTGCTGGAAAAGTCCAGCAAACTGAGATTTATGAGAAAGCAACATCAA	1544	PR 30-APR-1999; 990US-0132048.		
Qy	1317	GAGGGAGAAATTCTGTATGA-TGCAAGAACTGGACTCTG-CT	1374	PR 30-APR-1999; 990US-0132407.		
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Qy	1375	AGTAGATGCCCTGT---TAACAGCGCTGCTGTATGCCAAAGATATGGACGAGAT	1430	PR 06-MAY-1999; 990US-0132485.		
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Qy	1431	TGAAGCCACGACTACACAACCTTCACAGGAGGGCTTATGTTAGCAAGC	1489	PR 06-MAY-1999; 990US-0132487.		
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